

### Abstract 13:

Evolutionary changes of a low pathogenic avian influenza virus (H9N2) in poultry under the selective pressure from inactivated vaccine

Hongrui Cui<sup>1\*</sup>, Monique van Oers<sup>2</sup>, Nancy Beerens<sup>3</sup>, Mart C.M. de Jong<sup>1</sup>

<sup>1</sup> Quantitative Veterinary Epidemiology, Animal Sciences Group, Wageningen University & Research, The Netherlands

<sup>2</sup> Laboratory of Virology, Plant Science Group, Wageningen University & Research, The Netherlands

<sup>3</sup> Wageningen Bioveterinary Research, Wageningen University & Research, Lelystad, the Netherlands.

\* Corresponding author. E-mail: hongrui.cui@wur.nl

H9N2 subtype avian influenza virus (AIV) has become endemic in poultry in several location over the world, however, it was not under the primary surveillance and control in many countries due to its low pathogenicity. Several recent outbreaks of H9N2 in vaccinated poultry in Asian countries triggered the question on its transmission dynamics and evolutionary properties under the selective pressure from vaccination.

In this research, we first mimicked the natural infection and transmission process of H9N2 virus in vaccinated and non-vaccinated chickens. The statistical (S-I-R) model indicated that the transmission is not sufficiently reduced by the inactivated H9N2 vaccine. The estimated reproduction ratio (R) in non-vaccinated and low-vaccinated chicken (antisera HIT<8) were above 1. Even with higher titers (HIT>8) virus shedding still existed which contributed to the transmission in vaccinated chicken.

We therefore analysed surveillance samples that collected from local markets in 9 provinces in south China between 2013 and 2018. The H9N2 AIV isolated after 2013 grouped into a distinct new antigenic cluster, showing more mutations and a larger antigenic distance from vaccine strains (1998). Specific amino acid mutations were identified that could be related to the antigenic changes. Our findings were based on the available surveillance information of H9N2 AIV in local markets in China during 2013-2018. However, the combination of phylogenetic and antigenic analysis gave new insights to understand the molecular changes associated with antigenic drift.